Early Detection of Chronic Kidney Diseaseusing Machine learning

IBM PROJECT

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Introduction to Chronic Kidney disease

Chronic kidney disease (CKD) means your kidneys are damaged and can't filter blood the way they should. The disease is called "chronic" because the damage to your kidneys happens slowly over a long period of time. This damage can cause wastes to build up in your body. CKD can also cause other health problems.

The kidneys' main job is to filter extra water and wastes out of your blood to make urine. To keep your bodyworking properly, the kidneys balance the salts and minerals—such as calcium, phosphorus, sodium, and potassium—that circulate in the blood. Your kidneys also make hormones that help control blood pressure, make red blood cells, and keep your bones strong.

Kidney disease often can get worse over time and may lead to kidney failure. If your kidneys fail, you will need dialysis or a kidney transplant to maintain your health.

The sooner you know you have kidney disease, the sooneryou can make changes to protect your kidneys.

The kidneys' main job is to filter extra water and wastes out of your blood to make urine. To keep your body working properly, the kidneys balance the salts and minerals—such as calcium, phosphorus, sodium, and potassium—that circulate in the blood. Your kidneys also make hormones that help control blood pressure, make red blood cells, and keep your bones strong.

PROJECT OVERVIEW:

The main goal of treatment is to prevent progression

CKD to complete kidney failure. The best way to do thisis to diagnose CKD early and control the underlying cause. The symptoms, evaluation, and management of CKD will be reviewed here. To detect the detection of disease at the earliest stage of spread of disease. To provide correct accuracy of spread of disease. To preventspread of disease at the early stage.

PURPOSE:

- To detect the disease spread in the early stage
- To prevent the loss of life and to prevent the kidneyfailure.
- To estimate the accuracy of chronic kidney disease.
- To save the time and to detect in an easier way.
- Your test results can be used to determine howdamaged your kidneys are known as the stage of ckd.
- To prevent side effects of ckd such as breathing.

LITERATURE SURVEY OF CHRONIC KIDNEYDISEASE ANALYSIS:

SURVEY 1:

STATISTICAL AND DATA MINING ASPECTS ON KIDNEY STONES: A SYSTEMATIC REVIEW AND META ANALYSIS:

This project is about a systematic review and meta-analysis using classification algorithms studies detectedgood accuracy with C4.5, classification tree and Randomforest(93%) followed by Support Vector Machines(SVM)(91.98%).Logistic and NNge has alsoshown good accuracy results also shown good accuracy Results with zero relative absolute error and 100%correctly classified results. Machine Learning approachesmay provide better results in the treatment of kidneystones. Data mining offers a more quantative approach toquality control with ,user friendly for clinicians inreading the reports and reduce the errors. A meta-analysiscombines results of a number of studies that deal with a set of related research hypotheses. A meta-analysis may be conducted on a several clinical trials of a medical treatment which refer to statistical methods combining evidence. In the present experimentation, we had analyzed a setoff parameters related to kidney stone formation collected from patients in kaviti, and Andhra Pradesh, India.

SURVEY 2:

DETECTION OF CHRONIC KIDNEY DISEASEUSING RANDOM FOREST MACHINE LEARNING ALGORITHM:

In this paper they have used random forest machine learning algorithm to detect the chronic kidney disease they have compared the performance of six classifiers in the detection of chronic kidney disease analysis. The experimental results of the proposed method have demonstrated the RF has produced superior detection performance in terms of classification accuracy. AUC andMCC respectively for our considered dataset. It was also observed that few classifiers have yielded poorclassification accuracy as compared to RF like SMO and RBF.

SURVEY 3:

A NOVEL DETECTION FOR KIDNEY DISEASE USING IMPROVED SUPPORT VECTOR MACHINE:

This paper is about a novel detection for kidney disease using improved support vector machine. In this work, kidney disease detection system was developed using classification algorithms(KNN, Naive Bayes, SVM, ISVM) through MATLAB data mining tool to detect effective and better accurate results regarding whether thepatient is suffering from kidney disease or not. As the kidney disease patients are increasing world- wide each year and huge amounts of data is available for research, where different data mining techniques are used in the diagnosis of kidney disease. Different attributes are used for detection of kidney disease.

SURVEY 4:

DATA MINING CLASSIFICATION ALGORITHMS FOR KIDNEY DISEASE DETECTION:

In this paper data mining classification algorithm for kidney disease detection naive Bayes, svm, Ann, anfis they have used kidney function test (KFT) dataset. The algorithm which has the higher accuracy with the minimum execution time has chosen as the best algorithm machine learning tool is resulting in high Classification accuracy rate. The gap identified in the classifiers show different accuracy rate. Data mining is an approach which dispense an intermixture of technique to identify a block of data or decision making knowledge in the database and eradicating these data in such a way that they can be put to use in decision support, forecasting and estimation.

REFERENCES

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- Alijaaf AJ, AI-jumeily D, Haglan HM, Alloghani M,

Basker T, et al. (2018) Early Detection of chronic kidney using machine learning supported by detective analytics. 2018 IEEE Congress on Evolutionary Computation (CEC).

- Avci E,karakus S, Ozmen O, Avci(2018)PerformanceComparison of Some Classifiers on Chronic Kidney Disease Data. 2018 6th International Symposium on Digital Forensic and Security (ISDFS).

Problem statement Definition:

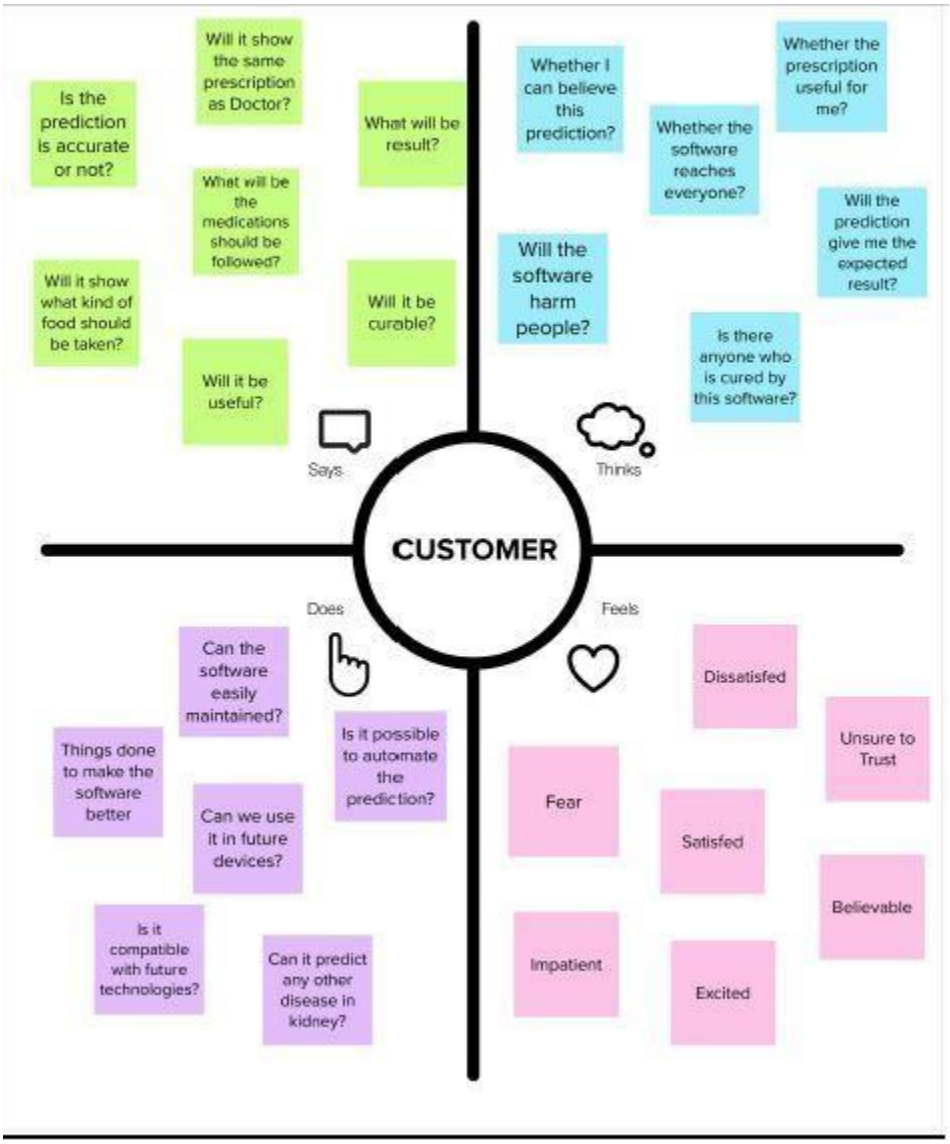
Our customer is a person who is suffering from breathing problems. He wishes to know whether there is spread of disease because breathing problem is a side effect or symptoms of kidney disease. He has too some test and he wishes to know the presence of disease using the given data. If there is a spread of disease, if yes he has to consult a doctor else he can feel free and satisfied. Due to the customer is very aged he cannot go to hospital and wants to detect in a simple manner.

The detection of disease can be done by using classification and regression methods.

IDEATION AND PROPOSED SOLUTION

Empathy Map Canvas:

An empathy map is a collaborative tool teams can use to gain a deeper insight into their customers. Much like a user persona, an empathy map can represent a group of users, such as a customer segment. The empathy map was originally created by Dave Gray and has gained much popularity within the agile community.



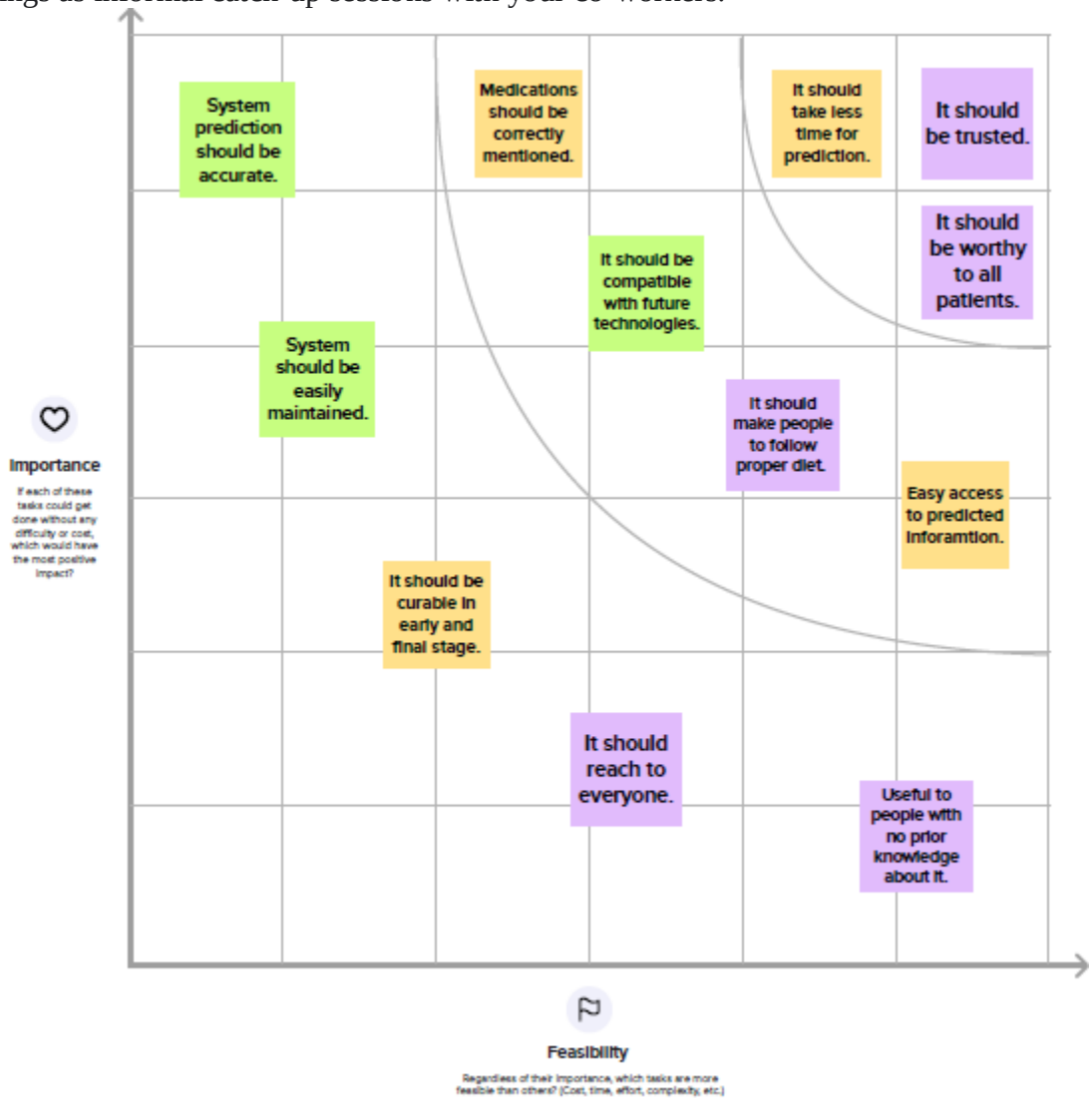
Ideation and Brainstorming:

Ideation:

Ideation is the process of forming ideas from conception to implementation, most often in a business setting. Ideation is expressed via graphical, written, orverbal methods, and arises from past or present knowledge, influences, opinions, experiences, and personal convictions

Brainstorming:

Brainstorming is a group activity where everyone comes together to discuss strategies for growth and improvement. You can exchange ideas, share important information and use these meetings as informal catch-up sessions with your co-workers.



Proposed Solution:

Proposed Solution means the combination of software, hardware, other products or equipment, and any and all services (including any installation, implementation, training, maintenance and support services) necessary to implement the solution described by Vendor in its Proposal.

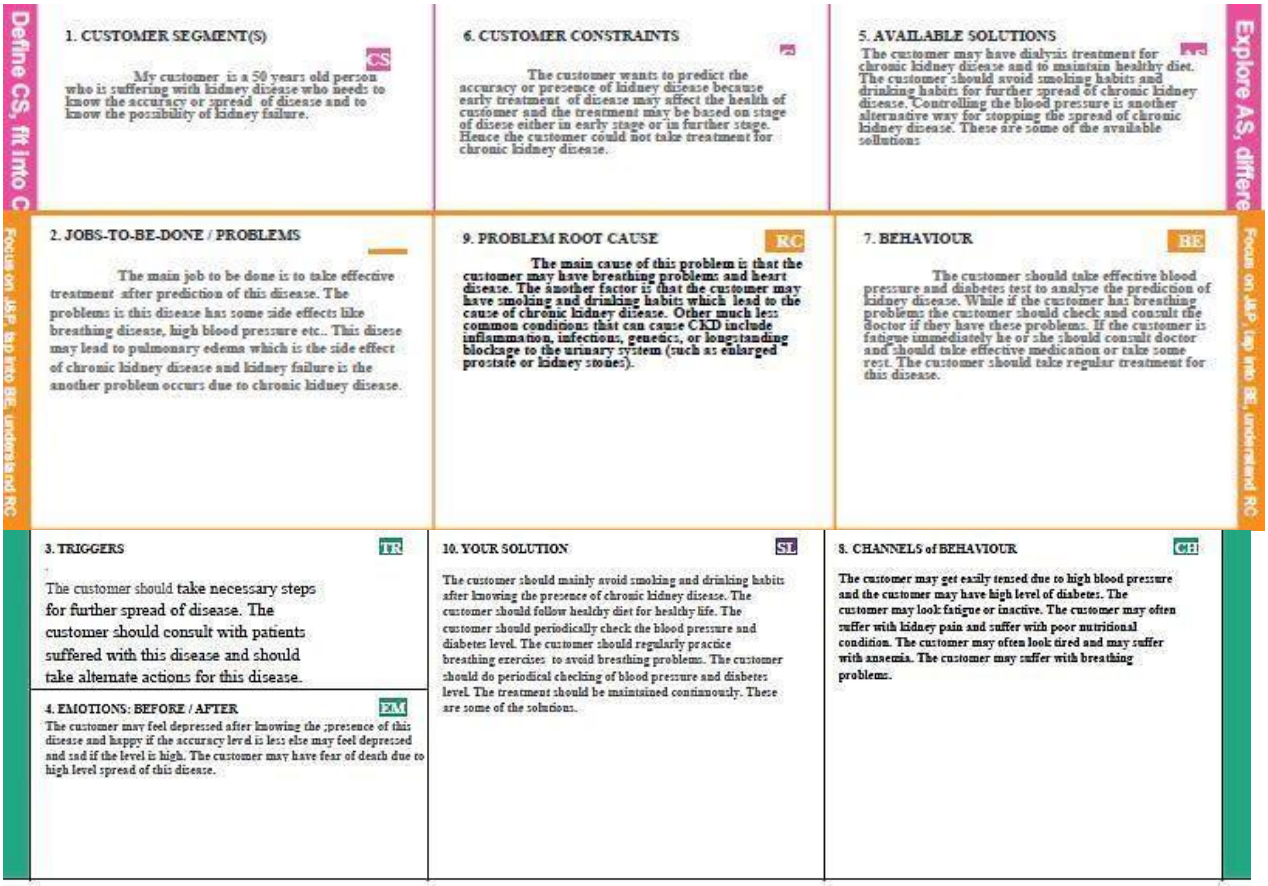
S.No	Parameter	Description
1.	Problem Statement (Problem to be solved)	The goal is to detect the presence of chronic kidney disease at the early stage of disease, so that the disease can be cured at the early stage and the prevention of loss of life can be done.
2.	Idea / Solution description	This concept is useful in medical field especially using this the disease can be detected easily and quicker manner. The detection of this disease may help many patients to prevent additional side effects like pulmonary edema which may lead to breathing problems and heart attacks

3.	Novelty / Uniqueness	Chances of kidney failure can be reduced and the disease can be cured. The side effects of the chronic kidney disease can be prevented by detecting at the early stage.
4.	Social Impact / Customer Satisfaction	It helps the doctors to detect the disease at the early stage and easier manner. It helps to preventloss of life and

		kidney failure.
5.	Scalability of theSolution	Supportful in detection of disease and side effects of kidney disease.

Problem Solution Fit:

The Problem-Solution Fit simply means that you have found a problem with your customer and that the solution you have realized for it actually solves the customer's problem.



REQUIREMENT ANALYSIS:

Requirements analysis, also called requirements engineering, is the process of determining user expectations for a new or modified product. In software engineering, it is sometimes referred to loosely by names such as requirements gathering or requirements capturing.

TYPES OF REQUIREMENTS:

1. Functional Requirements.
2. Non-functional Requirements.

Functional Requirements:

Functional requirements define what a product mustdo, what its features and functions are.

- Home page.
- Detection page.
- Result page.
- Anaconda prompt.

Non-Functional Requirements:

Non-functional requirements are global constraints on a software system are e.g., development costs, operational costs, performance, reliability, maintainability, portability, robustness etc.

Some of the non-functional requirements are,

- Security
- Reliability
- Compatibility
- Environment friendly
- Maintainability
- Usability

PROJECT DESIGN:

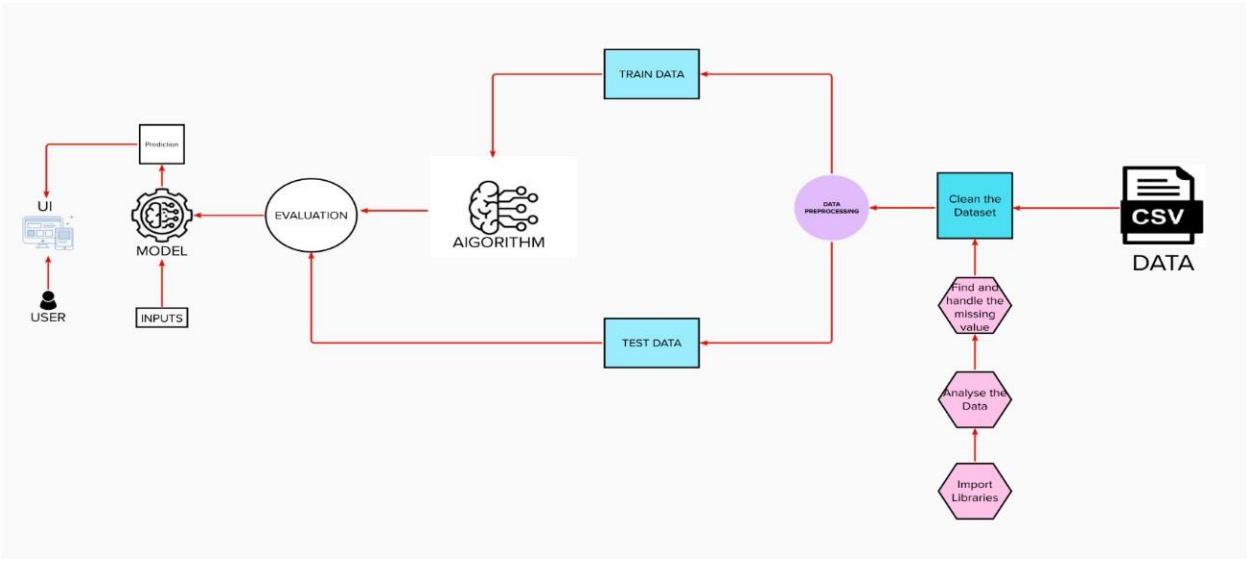
Project design is an early phase of the project lifecycle where ideas, processes, resources, and deliverables are planned out. A project design comes before a project plan as it's a broad overview whereas a project plan includes more detailed information.

TOPICS IN PROJECT DESIGN:

- DATA FLOW DIAGRAMS.
- SOLUTION AND TECHNICAL ARCHITECTURE.
- USER STORIES.

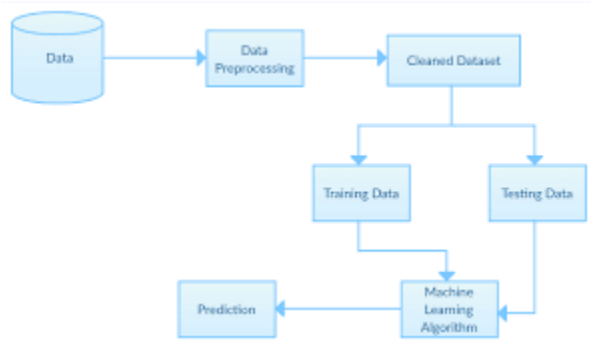
DATA FLOW DIAGRAMS:

A data flow diagram (DFD) maps out the flow of information for any process or system. It uses defined symbols like rectangles, circles and arrows, plus short text labels, to show data inputs, outputs, storage points and theroutes between each destination.



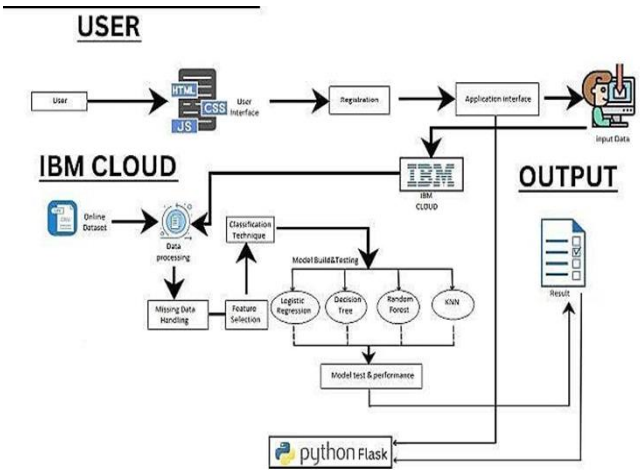
SOLUTION AND TECHNICAL ARCHITECTURE:SOLUTION ARCHITECTURE:

A solution architecture (SA) is an architectural description of a specific solution. SAs combine guidance from different enterprise architecture viewpoints (business, information and technical), as well as from the enterprise solution architecture.



TECHNICAL ARCHITECTURE:

Technical architecture—which is also often referred to as application architecture, IT architecture, businessarchitecture, etc., refers to creating a structured software solution that will meet the business needs and expectations while providing a strong technical plan for the growth of the software application through itslifetime.



USER STORIES:

- A user story is an informal, general explanation of a software feature written from the perspective of the end user or customer. The purpose of a user story is to articulate how a piece of work will deliver a particular value back to the customer.

- Ex: As a customer, I want to know the spread of the kidney disease. By entering the values like red blood count, pulmonary edema values I can know the accuracy of spread of disease.

- As a user, I can identify the disease easier.

- As a user, I can detect from diabetes as perprescription.

- As a user, I can use it to clearly identify thekidney stones.

PROJECT PLANNING AND SCHEDULING:

PROJECT PLANNING:

Project planning is a discipline addressing how to complete a project in a certain timeframe, usually with defined stages and designated resources. One view of project planning divides the activity into these steps: setting measurable objectives. identifying deliverables. scheduling.

SCHEDULING:

Scheduling is the process of arranging, controlling and optimizing work and workloads in a production process or manufacturing process. Scheduling is used to allocate plant and machinery resources, plan human resources, plan production processes and purchase materials.

SPRINT PLANNING:

Sprint Planning is an event that defines what can be delivered in the upcoming Sprint and how their work can be achieved. It kicks off the Sprint.

Each Sprint has a specific duration.

- Sprint 1-Data Collection.
- Sprint 2- Model Building.
- Sprint 3- Training and Testing.
- Sprint 4- Implementation of the Application.

ESTIMATION:

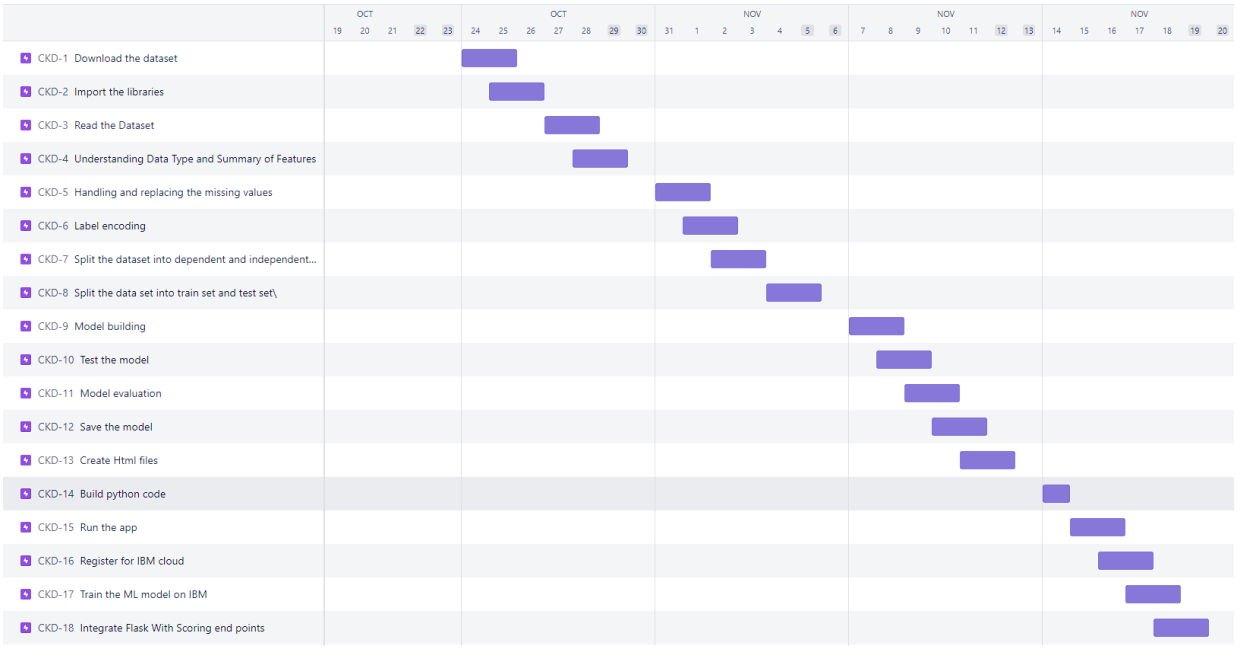
Estimation is a process to detect the time and the costthat a project requires to be finished appropriately.

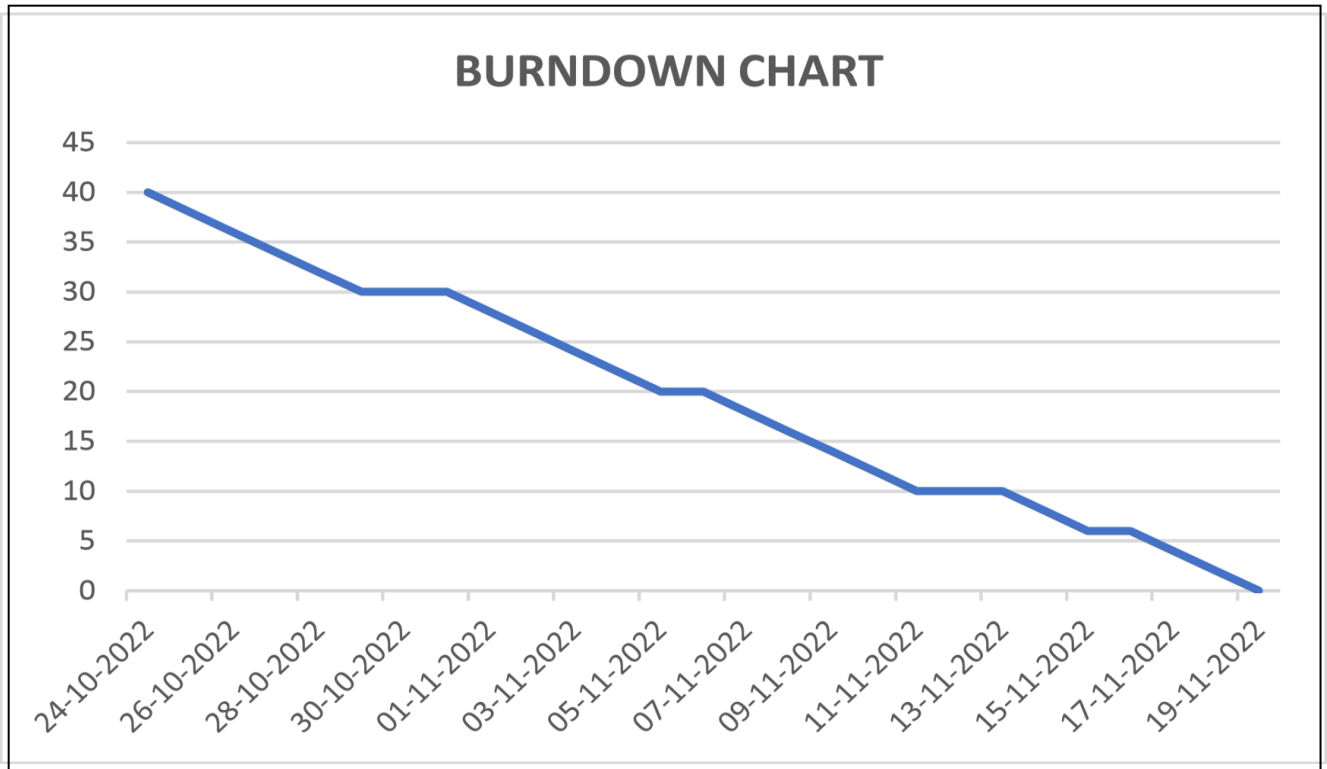
SPRINT DELIVERY SCHEDULE:

Sprint Delivery Schedule is the process of describingthe duration of each sprint and the delivery of each sprint is called sprint delivery schedule.

Sprint	Sprint Start Date	Sprint End Date	Sprint Release Date
Sprint-1	24 Oct 2022	29 Oct 2022	29 Oct 2022
Sprint-2	31 Oct 2022	05 Nov 2022	05 Nov 2022
Sprint-3	07 Nov 2022	12 Nov 2022	12 Nov 2022
Sprint-4	14 Nov 2022	19 Nov 2022	19 Nov 2022

REPORTS FROM JIRA:





CODING AND SOLUTIONING:

Coding or programming is the key activity and an engineering methodology through which the systemvisualized by the end user in terms of requirements is brought to life.

Solutioning is the process of acquiring the solution to the given problem is called as Solutioning.

FEATURE 1:

The main feature used in the coding is the machine learning concept. This machine learning is mainly used for detection of accuracy of disease.

Machine learning is a subfield of artificial intelligence, which is broadly defined as the capability ofa machine to imitate intelligent human behavior.

FEATURE 2:

The second main feature used in coding is the Regression model.

Logistic Regression model is used for detection ofthe chronic kidney disease.

Logistic regression aims to solve classification problems. It does this by detecting categorical outcomes, unlike linear regression that detects a continuous outcome. In the simplest case there are two outcomes, which is called binomial, an example of which is detecting if a tumor is malignant or benign.

```
from sklearn.linear_model import LogisticRegression
lgr = LogisticRegression()
lgr.fit(x_train,y_train)
```

TESTING:

Testing is the practice of making objective judgments regarding the extent to which the. system (device) meets, exceeds or fails to meet stated objectives.

TEST CASES:

A test case is a set of actions performed on a system to determine if it satisfies software requirements and functions correctly

TEST SCENARIOS:

- Verify whether is able to enter data to detection ofaccuracy of disease.
- Verify whether the user is getting the correct accuracy of disease.
- Verify whether the environment is user friendly ornot.

USER ACCEPTANCE TESTING:

User acceptance testing (UAT), also called application testing or end-user testing, is a phase of software development in which the software is tested in the real world by its intended audience.

It involves testing the entire software and detecting the errors, measuring the level of security, environment friendly software etc.

RESULTS:

- Performance Metrics:

Performance metrics are defined as figures and data representative of an organization's actions, abilities, and overall quality.

- Label Encoding:

Label Encoding refers to converting the labels intoa numeric form so as to convert them into the machine- readable form

```
from sklearn.preprocessing import LabelEncoder # importing Labelencoding from sklearn
for i in catcols: # looping through all the categorical column
  print("LABEL ENCODING OF:",i)
  LEi = LabelEncoder() # creating an object of labelencoder
  print(c(data[i])) # getting the classes values before transformation
  data[i] = LEi.fit_transform(data[i]) # transfering our test classes to numerical values
  print(c(data[i])) # getting the classes values after transformation
  print("*"*100)
```

.

- Independent and Dependent Variables:

A dependent variable is a variable whose value depends on another variable, whereas An Independentvariable is a variable whose value never depends on another variable.

```
selcols=['red_blood_cells','pus_cell','blood glucose random','blood_urea','pedal_edema','anemia','diabetesmellitus','coronary_artery_disease']
x=pd.DataFrame(data,columns=selcols)
y=pd.DataFrame(data,columns=['class'])
print(x.shape)
print(y.shape)
```

- Build The Model:

Model building is the process of developing a probabilistic model that best describes the relationshipbetween the dependent and independent variables.

```
from sklearn.linear_model import LogisticRegression
lgr = LogisticRegression()
lgr.fit(x_train,y_train)
```

- Accuracy Score Of The Model:

It is the process of detecting the accuracy score ofthe model.

```
accuracy_score(y_test,y_pred)
```

```
0.8625
```

- Confusion Matrix of our Model:

A Confusion matrix is an N x N matrix used for evaluating the performance of a classification model, where N is the number of target classes.

```
conf_mat = confusion_matrix(y_test,y_pred)
conf_mat
```

```
array([[40, 10],
       [ 1, 29]])
```

ADVANTAGES AND DISADVANTAGES:

ADVANTAGES:

- The early detection of CKD allows patients to receive timely treatment, slowing the disease's progression.
- Due to its rapid recognition performance and accuracy, machine learning models can effectivelyassist physicians in achieving this goal.
- To prevent the kidney failure.
- To prevent loss of life.
- Using this we an able to detect at the early stage and the patient can take efficient treatment according to the spread.

DISADVANTAGES:

- Sometimes the accuracy may vary.
- The result may vary if the accuracy value is wrongor vary.

These are some of the advantages of disadvantages ofchronic kidney disease analysis using machine learning.

CONCLUSION:

Chronic renal failure represents a critical period in the evolution of chronic renal disease and is associated with complications and comorbidities that begin early in the course of the disease. These conditions are initially subclinical but progress relentlessly and may eventually become symptomatic and irreversible. Early in the course of chronic renal failure, these conditions are amenable to interventions with relatively simple treatments that have the potential to prevent adverse outcomes.6 Globally, CKD is most commonly attributed to diabetes and/or hypertension, but other causes such as glomerulonephritis, infection, and environmental exposures (such as air pollution, herbal remedies, and pesticides) are common in Asia, sub-Saharan Africa, and many developing countries.4 Genetic risk factors may also contribute to CKD risk. For example, sickle cell trait and the presence of 2 APOL1 risk alleles, both common in people of African ancestry but not European ancestry, may double the risk of CKD.4,7–10

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FUTURE SCOPE:

- In future, it can be used in hospitals.
- It can be used at medical fields for easy detection ofkidney disease at the early stage.
- It can be used as a web service for detection usingonline.
- It can be used to develop an application which maybe helpful for detection of disease at the easiest way.
- For old age people it is very helpful to detect thedisease.
- Easy way of detection of kidney disease.

APPENDIX:

A document that describes the design of a softwarecomponent, product, or system.

SOURCE CODE:

```
# Importing Libraries
```

+ Code + Text

```
[ ] import pandas as  pd # used for data manipulation
    import numpy as np  # used for numerical analysis
    from collections import Counter as c # return counts of number of classess
    import matplotlib.pyplot as plt # used for data visualization
    import seaborn as sns # data visualization library
    import missingno as msno # finding missing values
    from sklearn.metrics import accuracy_score,confusion_matrix # model performance
    from sklearn.model_selection import train_test_split # splits data in random train and test array
    from sklearn.preprocessing import LabelEncoder # encoding the levels of categorical features
    from sklearn.linear_model import LogisticRegression # classification ml algorithm
    import pickle # python object hierarchy is converted into byte stream
```

```
[ ] # loading the dataset
```

```
[ ] data=pd.read_csv('/content/drive/MyDrive/Datasets/chronickidneydisease.csv')
```

```
[ ] data.head() # return you the first 5 rows values
```

+ Code + Text

```
[ ] data.head() # return you the first 5 rows values
```

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	...	44	7800	5.2	yes	yes	no	good	no	no	ckd
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	...	38	6000	NaN	no	no	no	good	no	no	ckd
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31	7500	NaN	no	yes	no	poor	no	yes	ckd
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32	6700	3.9	yes	no	no	poor	yes	yes	ckd
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35	7300	4.6	no	no	no	good	no	no	ckd

5 rows × 26 columns

```
[ ] data.tail() # return you the last 5 rows values
```

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
395	395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	47	6700	4.9	no	no	no	good	no	no	notckd
396	396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	54	7800	6.2	no	no	no	good	no	no	notckd
397	397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	...	49	6600	5.4	no	no	no	good	no	no	notckd
398	398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	51	7200	5.9	no	no	no	good	no	no	notckd
399	399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	...	53	6800	6.1	no	no	no	good	no	no	notckd

```
data.head(10) # return the first 10 rows values
```

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	...	pcv	wc	rc	htn	dm	cad	appet	pe	ane	classification
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	...	44	7800	5.2	yes	yes	no	good	no	no	ckd
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	...	38	6000	NaN	no	no	no	good	no	no	ckd
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	...	31	7500	NaN	no	yes	no	poor	no	yes	ckd
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	...	32	6700	3.9	yes	no	no	poor	yes	yes	ckd
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	...	35	7300	4.6	no	no	no	good	no	no	ckd
5	5	60.0	90.0	1.015	3.0	0.0	NaN	NaN	notpresent	notpresent	...	39	7800	4.4	yes	yes	no	good	yes	no	ckd
6	6	68.0	70.0	1.010	0.0	0.0	NaN	normal	notpresent	notpresent	...	36	NaN	NaN	no	no	no	good	no	no	ckd
7	7	24.0	NaN	1.015	2.0	4.0	normal	abnormal	notpresent	notpresent	...	44	6900	5	no	yes	no	good	yes	no	ckd
8	8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	present	notpresent	...	33	9600	4.0	yes	yes	no	good	no	yes	ckd
9	9	53.0	90.0	1.020	2.0	0.0	abnormal	abnormal	present	notpresent	...	29	12100	3.7	yes	yes	no	poor	no	yes	ckd

10 rows × 26 columns

```
data.drop(["id"],axis=1,inplace=True) # drop is used for drop the column
```

```
data.columns # return all the column names
```

```
data.columns # return all the column names
```

```
Index(['age', 'bp', 'sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'bgr', 'bu',
       'sc', 'sod', 'pot', 'hemo', 'pcv', 'wc', 'rc', 'htn', 'dm', 'cad',
       'appet', 'pe', 'ane', 'classification'],
      dtype='object')
```

```
data.columns=['age','blood_pressure','specific_gravity','albumin','sugar','red_blood_cells','pus_cell','pus_cell_clumps','bacteria','blood glucose random',
'blood_urea','serum_creatinine','sodium','potassium','hemoglobin','packed_cell_volume','white_blood_cell_count','red_blood_cell_count','hypertension',
'diabetesmellitus','coronary_artery_disease','appetite','pedal_edema','anemia','class'] # manually giving the name of the columns
data.columns
```

```
Index(['age', 'blood_pressure', 'specific_gravity', 'albumin', 'sugar',
       'red_blood_cells', 'pus_cell', 'pus_cell_clumps', 'bacteria',
       'blood glucose random', 'blood_urea', 'serum_creatinine', 'sodium',
       'potassium', 'hemoglobin', 'packed_cell_volume',
       'white_blood_cell_count', 'red_blood_cell_count', 'hypertension',
       'diabetesmellitus', 'coronary_artery_disease', 'appetite',
       'pedal_edema', 'anemia', 'class'],
      dtype='object')
```

```
data.info() # info will give you a summary of dataset
```

```
# Target Column
```

```
data['class'].unique() # find the unique elements of an array
```

```
array(['ckd', 'ckd\t', 'notckd'], dtype=object)
```

```
# Rectifying the Target Column
```

```
data['class']=data['class'].replace("ckd\t","ckd") # replace is used for renaming
data['class'].unique()
```

```
array(['ckd', 'notckd'], dtype=object)
```

```
catcols = set(data.dtypes[data.dtypes =='O'].index.values) # only fetch the object type columns
print(catcols)
```

```
{'hypertension', 'class', 'red_blood_cell_count', 'anemia', 'pus_cell_clumps', 'white_blood_cell_count', 'diabetesmellitus', 'pedal_edema', 'red_blood_cells', 'ba
```

```
for i in catcols:
    print("Columns :",i)
    print(c(data[i])) # using counter for checking the number of classess in the column
    print('*'*120+'\n')
```

```
[ ] # Removing the Columns which are not Numerical
```

```
[ ] # Categorical Column
```

```
[ ] catcols.remove('red_blood_cell_count')
    catcols.remove('packed_cell_volume')
    catcols.remove('white_blood_cell_count')
    print(catcols)
```

```
{'hypertension', 'class', 'anemia', 'pus_cell_clumps', 'diabetesmellitus', 'pedal_edema', 'red_blood_cells', 'bacteria', 'coronary_artery_disease', 'pus_cell', 'a
```

```
[ ] # Numerical Columns
```

```
[ ] contcols=set(data.dtypes[data.dtypes!='O'].index.values) # only fetch the float and int type columns
    contcols=pd.DataFrame(data,columns=contcols)
    print(contcols)
```

```
[ ] contcols.remove('specific_gravity')
    contcols.remove('albumin')
    contcols.remove('sugar')
    print(contcols)
```

```
{'blood_pressure', 'serum_creatinine', 'sodium', 'blood glucose random', 'blood_urea', 'age', 'hemoglobin', 'potassium'}
```

```
[ ] # Adding columns which we found continuous
```

```
[ ] contcols.add('red_blood_cell_count') # using add we can add the column
    contcols.add('packed_cell_volume')
    contcols.add('white_blood_cell_count')
    print(contcols)
```

```
{'blood_pressure', 'serum_creatinine', 'sodium', 'red_blood_cell_count', 'blood glucose random', 'white_blood_cell_count', 'blood_urea', 'age', 'hemoglobin', 'pac
```

```
[ ] # Adding columns which we found Categorical
```

```
[ ] catcols.add('specific_gravity')
    catcols.add('albumin')
    catcols.add('sugar')
    print(catcols)
```

```
[ ] # Rectifying the Categorical column classes
```

```
[ ] data['coronary_artery_disease'] = data.coronary_artery_disease.replace('\tno','no') # replacing \tno with no
    c(data['coronary_artery_disease'])
```

```
Counter({'no': 364, 'yes': 34, nan: 2})
```

```
[ ] data['diabetesmellitus'] = data.diabetesmellitus.replace(to_replace={'\tno':'no','\tyes':'yes','yes':'yes'})
    c(data['diabetesmellitus'])
```

```
Counter({'yes': 136, 'no': 261, ' yes': 1, nan: 2})
```

```
[ ] # Null Values
```

```
[ ] data.isnull().any() # it will return true if any missing values
```

```
data.isnull().sum() # returns the count of missing values
```

```
[ ]
```

```
[ ] # Handling Continuous/numerical colunmns null values
```

```
data['blood glucose random'].fillna(data['blood glucose random'].mean(),inplace=True)
data['blood_pressure'].fillna(data['blood_pressure'].mean(),inplace=True)
data['blood_urea'].fillna(data['blood_urea'].mean(),inplace=True)
data['hemoglobin'].fillna(data['hemoglobin'].mean(),inplace=True)
data['packed_cell_volume'].fillna(data['packed_cell_volume'].mean(),inplace=True)
data['potassium'].fillna(data['potassium'].mean(),inplace=True)
data['red_blood_cell_count'].fillna(data['red_blood_cell_count'].mean(),inplace=True)
data['serum_creatinine'].fillna(data['serum_creatinine'].mean(),inplace=True)
data['sodium'].fillna(data['sodium'].mean(),inplace=True)
data['white_blood_cell_count'].fillna(data['white_blood_cell_count'].mean(),inplace=True)
```

```
[ ] data['age'].fillna(data['age'].mode()[0],inplace=True)
    data['hypertension'].fillna(data['hypertension'].mode()[0],inplace=True)
    data['pus_cell_clumps'].fillna(data['pus_cell_clumps'].mode()[0],inplace=True)
    data['appetite'].fillna(data['appetite'].mode()[0],inplace=True)
    data['albumin'].fillna(data['albumin'].mode()[0],inplace=True)
    data['pus_cell'].fillna(data['pus_cell'].mode()[0],inplace=True)
    data['red_blood_cells'].fillna(data['red_blood_cells'].mode()[0],inplace=True)
    data['coronary_artery_disease'].fillna(data['coronary_artery_disease'].mode()[0],inplace=True)
    data['bacteria'].fillna(data['bacteria'].mode()[0],inplace=True)
    data['anemia'].fillna(data['anemia'].mode()[0],inplace=True)
    data['sugar'].fillna(data['sugar'].mode()[0],inplace=True)
    data['diabetesmellitus'].fillna(data['diabetesmellitus'].mode()[0],inplace=True)
    data['pedal_edema'].fillna(data['pedal_edema'].mode()[0],inplace=True)
    data['specific_gravity'].fillna(data['specific_gravity'].mode()[0],inplace=True)
```

```
[ ] data.isnull().sum()
```

```
[ ] # Label Encoding
```

```
[ ] from sklearn.preprocessing import LabelEncoder # importing Labelencoding from sklearn
    for i in catcols: # looping through all the categorical column
      print("LABEL ENCODING OF:",i)
      LEi = LabelEncoder() # creating an object of labelencoder
      print(c(data[i])) # getting the classes values before transformation
      data[i] = LEi.fit_transform(data[i]) # transfering our test classes to numerical values
      print(c(data[i])) # getting the classes values after transformation
      print("*"*100)
```

```
# Creating Independent and Dependent
```

+ Code + Text

```
[ ] selcols=['red_blood_cells','pus_cell','blood glucose random','blood_urea','pedal_edema','anemia','diabetesmellitus','coronary_artery_disease']
    x=pd.DataFrame(data,columns=selcols)
    y=pd.DataFrame(data,columns=['class'])
    print(x.shape)
    print(y.shape)
```

```
(400, 8)
(400, 1)
```

```
[ ] # Splitting the Data into train and test
```

```
[ ] from sklearn.model_selection import train_test_split
    x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2,random_state=None) # train test split the data
```

```
[ ] print(x_train.shape)
    print(y_train.shape)
    print(x_test.shape)
    print(y_test.shape)
```

```
# Build the Model
```

```
from sklearn.linear_model import LogisticRegression
lgr = LogisticRegression()
lgr.fit(x_train,y_train)
```

```
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:993: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please c
  y = column_or_1d(y, warn=True)
/usr/local/lib/python3.7/dist-packages/sklearn/linear_model/_logistic.py:818: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG,
LogisticRegression()
```

```
# Predicting our output with the model which we build
```

```
y_pred = lgr.predict(x_test)
```

```
# Accuracy score of Model
```

```
accuracy_score(y_test,y_pred)
```

```
0.8625
```

```
# Confusion Matrix of our Model
```

```
conf_mat = confusion_matrix(y_test,y_pred)
conf_mat
```

```
array([[40, 10],
       [ 1, 29]])
```

```
%cd /content/drive/MyDrive/Datasets
```

```
/content/drive/MyDrive/Datasets
```

```
#Dumping our model
pickle.dump(lgr, open('CKD.pk1','wb'))
```

Github Project Link:

https://github.com/IBM-EPBL/IBM-Project-18220-1659681273